

|  |   |                                 |
|--|---|---------------------------------|
| FORM PTO-1449<br><b>INFORMATION DISCLOSURE STATEMENT</b> | ATTY. DOCKET NO.<br><b>034263.002</b><br><b>(08899871US1)</b> | SERIAL NO.<br><b>10/598,140</b> |
|  | <b>Petronis et al.</b>  |                                 |
|  | FILING DATE<br><b>18 August 2006</b>                          | GROUP ART UNIT<br><b>1600</b>   |

### U.S. PATENT DOCUMENTS

| *Examiner's Initials | DOCUMENT NUMBER | DATE | NAME | CLASS | SUB-CLASS | FILING DATE, IF APPROPRIATE |
|----------------------|-----------------|------|------|-------|-----------|-----------------------------|
|                      |                 |      |      |       |           |                             |

### FOREIGN PATENT DOCUMENTS

| *Examiner's Initials | DOCUMENT NUMBER | DATE | COUNTRY | CLASS | SUB-CLASS | TRANSLATION<br>YES NO |  |
|----------------------|-----------------|------|---------|-------|-----------|-----------------------|--|
|                      |                 |      |         |       |           |                       |  |

### OTHER INFORMATION (Including Author, Title, Date, Pertinent Pages, Etc.)

| *Examiner's Initials | Author, et al. (DATE) "Title", Book/Journal, X(X):pp-pp.   |
|----------------------|--|
|                      | Adorj an, P., et al., Tumour class prediction and discovery by microarray-based DNA methylation analysis. Nucleic Acids Res, 2002. 30(5): p. e21   |
|                      | Balog, R.P., et al., Parallel assessment of CpG methylation by two-color hybridization with oligonucleotide arrays. Anal Biochem, 2002. 309(2): p. 301-10  |
|                      | Bird, A.P., CpG-rich islands and the function of DNA methylation. Nature, 1986. 321(6067): p. 209-13   |
|                      | Chen C. et al. Methylation target array for rapid analysis of CpG island hypermethylation in multiple tissue genomes. Am J Pathol. July 2003. Vol. 163, No.1, Pages 37-45                              |
|                      | Frommer, M., et al., A genomic sequencing protocol that yields a positive display of 5-methylcytosine residues in individual DNA strands. PNAS USA, 1992. 89(5): p. 1827-31                            |
|                      | Gitan, R.S., et al., Methylation-specific oligonucleotide microarray: a new potential for high-throughput methylation analysis. Genome Res, 2002. 12(1): p. 158-64;                                    |
|                      | Hatada, I., et al., A microarray-based method for detecting methylated loci. J Hum Genet, 2002.47(8): p. 448-51  |
|                      | Hou, P., et al., A microarray to analyze methylation patterns of p16(Ink4a) gene 5'-CpG islands. Clin Biochem , 2003 . 36(3): p . 197-202  |
|                      | Kruger et al. McrB: a prokaryotic protein specifically recognizing DNA containing modified cytosine residues. EMBO J, 1995. 14(11): p. 2661- 9   |
|                      | Shi, H., et al., Triple analysis of the cancer epigenome: an integrated microarray system for assessing gene expression, DNA methylation, and histone acetylation. Cancer Res, 2003. 63(9): p. 2164-71 |
|                      | Stewart & Raleigh, Dependence of McrBC cleavage on distance between recognition elements . Biol Chem, 1998. 379(4-5): p. 611-6   |
|                      | Sutherland et al., McrBC: a multisubunit GTP-dependent restriction endonuclease. J Mol Biol , 1992. 225(2): p. 327-48  |

|   |                                    |
|---|------------------------------------|
| EXAMINER:<br><br>/Christopher Babic/  | DATE CONSIDERED:<br><br>02/09/2009 |
| *EXAMINER: Initial if reference considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant. |                                    |

|  |   |                                 |
|--|---|---------------------------------|
| FORM PTO-1449<br><b>INFORMATION DISCLOSURE STATEMENT</b> | ATTY. DOCKET NO.<br><b>034263.002</b><br><b>(08899871US1)</b> | SERIAL NO.<br><b>10/598,140</b> |
|  | <b>Petronis et al.</b>  |                                 |
|  | FILING DATE<br><b>18 August 2006</b>                          | GROUP ART UNIT<br><b>1600</b>   |

|  |  |
|--|--|
|  | Tompa, R., et al ., Genome-wide profiling of DNA methylation reveals transposon targets of CHROMOMETHYLASE3. Curr Biol, 2002 . 12(I): p. 65-8                                |
|  | Toyota, M., et al ., Identification of differentially methylated sequences in colorectal cancer by methylated CpG island amplification. Cancer Res, 1999. 59(10): p. 2307-12 |
|  | van Steensel et al., Chromatin profiling using targeted DNA adenine methyltransferase. Nat Genet, 2001. 27(3): p. 304-8  |
|  | van Steensel & Henikoff, Epigenomic profiling using microarrays. Biotechniques , 2003. 35(2): p. 346-50, 352-4, 356-7  |
|  | Yamada, Y. et al. A comprehensive analysis of allelic Methylation status of CpG islands on human chromosome 21q. Genome Res. February 2004, "vol.14, No.2, pages 247-266     |
|  | Yan, P.S., et al., Dissecting complex epigenetic alterations in breast cancer using CpG island microarrays. Cancer Res, 2001. 61(23): p. 8375-80                             |
|  | Yan, P.S., et al., Use of CpG island microarrays to identify colorectal tumors with a high degree of concurrent methylation. Methods, 2002. 27(2): p. 162-9                  |

|   |                                    |
|---|------------------------------------|
| EXAMINER:<br><br>/Christopher Babic/  | DATE CONSIDERED:<br><br>02/09/2009 |
| *EXAMINER: Initial if reference considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant. |                                    |